



Search  for

# ScanProsite

*Doesn't identify  
pre-pro-region*

*Analysis  
of Yersinia*

## Search a sequence against PROSITE

Sequence:

MRILQLILLA LATGLVGGET [RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA  
AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV  
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCENAYPG  
NITDTMVCAS VQEGGKDSCQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTKVCKYV  
DWIQETMKNN]

PROSITE Release 18.10, of 12-Oct-2003

>PDOC00001 PS00001 ASN\_GLYCOSYLATION N-glycosylation site [pattern] [Warning: pattern with a high probability of occurrence].

99 - 102 NNSL  
165 - 168 NITI  
181 - 184 NITD  
210 - 213 NQSL

>PDOC00005 PS00005 PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].

132 - 134 SsR  
160 - 162 TlR  
227 - 229 TrK  
246 - 248 TmK

>PDOC00006 PS00006 CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].

88 - 91 TatE  
167 - 170 TiiE  
190 - 193 SvqE

>PDOC00008 PS00008 MYRISTYL N-myristoylation site [pattern] [Warning: pattern with a high probability of occurrence].

14 - 19 GLvgGE  
82 - 87 GCeqTR  
194 - 199 GGkdSC  
220 - 225 GQdpCA

>PDOC00124 PS50240 TRYPSIN\_DOM Serine proteases, trypsin domain [profile].

15 - 248 LVGGETriikgfECKPHSQPWQAALFEKT-RLLCGATLIAPRWLLTAAHCLKPR-----Y  
IVHLGQHNLQKEEGCEQTRTATESFPHPGFNslpNKDHRNDIMLVKMASPV SITWAVRP

LTL--SSRCVTAGTSCSLISGWGSTSSPqLRLPHTLRCANITIIHQKC-ENAYPGNITDT  
MVCASVQEGGKDSCQGDSGGPLVC---NQSLQGIISWGqDPCAITRKPGVYTKVCKYVD  
WIQETMK

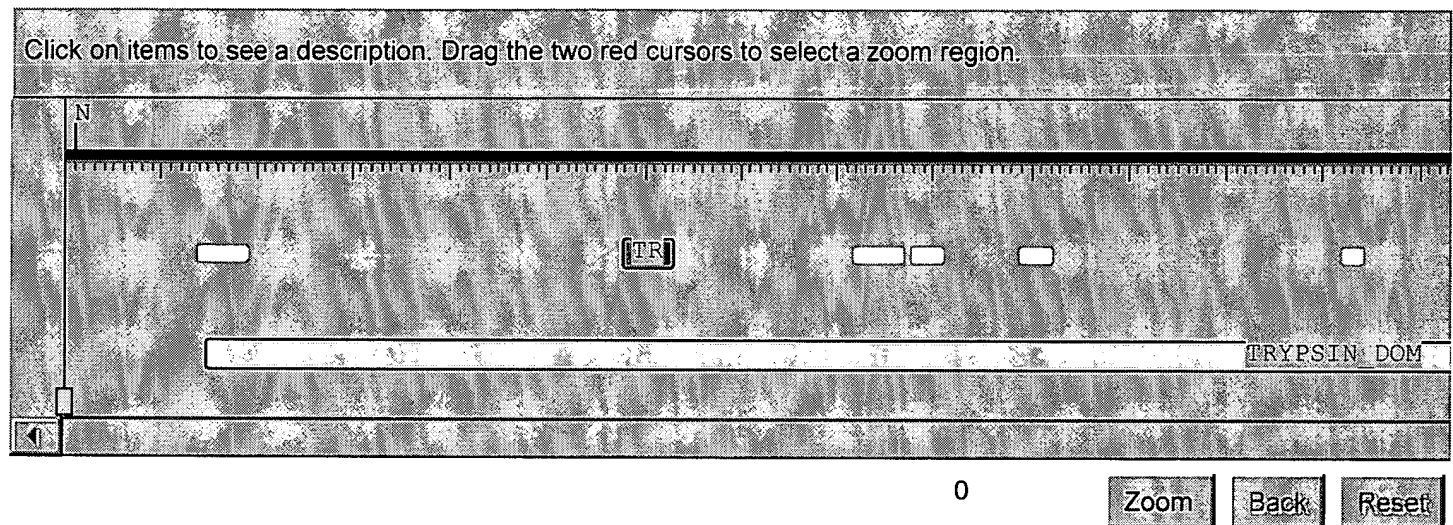
>PDOC00124 PS00134 TRYPSIN\_HIS Serine proteases, trypsin family, histidine active site [pattern].

58 - 63 LTA~~A~~H~~C~~

>PDOC00124 PS00135 TRYPSIN\_SER Serine proteases, trypsin family, serine active site [pattern].

197 - 208 DScqGDSGGPLV

### Graphical summary of hits (*java applet*)



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### Entry Information

Entry from: **SWALL**  
(SPTR)

### Entry Options

Launch analysis tool:

BlastP

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Link to related information:

[Link](#)

Save entry:

[Save](#)

View:

[Printer Friendly](#)[General](#) [Description](#) [References](#) [Comments](#) [Link](#)

### General information

Entry name **KLKB\_HUMAN**  
Accession number **Q9UBX7, O75837, Q9NS65**

Created Rel. 40, 16-OCT-2001

Sequence update Rel. 40, 16-OCT-2001

Annotation update Rel. 42, 15-SEP-2003

### Description and origin of the Protein

Description Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-  
Gene name(s) KLK11 OR PRSS20 OR TLSP.  
Organism source Homo sapiens (Human).  
Taxonomy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele  
Hominidae; Homo.  
NCBI TaxID 9606

### References

- [1] Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X.P., Shios  
**cdna cloning and expression of a novel serine proteas**  
(1998) *Biochim. Biophys. Acta* **1399**:225-228

Position SEQUENCE FROM N.A. (ISOFORM 1)

Comments TISSUE=Hippocampus;

Medline [98438738](#)PubMed [9765601](#)

- [2] Mitsui,S., Yamada,T., Okui,A., Kominami,K., Uemura,H., Yarr  
**A novel isoform of a kallikrein-like protease, TLSP/hip**  
**and prostate.**  
(2000) *Biochem. Biophys. Res. Commun.* **272**:205-211

Position SEQUENCE FROM N.A. (ISOFORMS 1

Comments TISSUE=Hippocampus, and Prostate

Medline [20329229](#)PubMed [10872828](#)

- [3] Yousef,G.M., Scorilas,A., Diamandis,E.P.,  
**Genomic organization, mapping, tissue expression, and**  
**(TLSP PRSS20), a new member of the human kallikreir**  
(2000) *Genomics* **63**:88-96

Position SEQUENCE FROM N.A. (ISOFORM 1)

Medline [20130117](#)PubMed [10662548](#)

- [4] Gan,L., Lee,I., Smith,R., Argonza-Barrett,R., Lei,H., McCuaig  
**Sequencing and expression analysis of the serine pr te**

Wouldn't know  
pep region till  
then.

	(2000) <i>Gene</i> <b>257</b> :119-130
	Position SEQUENCE FROM N.A. (ISOFORM 1)
	Medline <a href="#">20510030</a>
	PubMed <a href="#">11054574</a>
[5]	Lamerdin,J.E., McCready,P.M., Skowronski,E., Viswanathan,V, Stilwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A. Christensen,M., Georgescu,A., Avila,J., Liu,S., Andreise,T., Ti Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arella Olsen,A.S., Carrano,A.V., <b>Sequence analysis of chromosome 19q13.4.Submitted</b>
	Position SEQUENCE FROM N.A. (ISOFORM 1)
[6]	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klau Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaef Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farn Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., B Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A. Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketten Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., T Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S.N., Krz Schein,J.E., Jones,S.J.M., Marra,M.A., <b>Generation and initial analysis of more than 15,000 ful</b> (2002) <i>Proc. Natl. Acad. Sci. U.S.A.</i> <b>99</b> :16899-16903
	Position SEQUENCE FROM N.A. (ISOFORM 1)
	Comments TISSUE=Testis;
	Medline <a href="#">22388257</a>
	PubMed <a href="#">12477932</a>

**Comments****FUNCTION**

POSSIBLE MULTIFUNCTIONAL PROT  
BZ-PHE-ARG-4-METHYLCOUMARYL-  
OTHER SUBSTRATES FOR KALLIKRE

**SUBCELLULAR LOCATION**

SECRETED.

**ALTERNATIVE PRODUCTS**

Event=Alternative splicing; Named i  
Sequence=Displayed; Name=2; Iso:

**TISSUE SPECIFICITY**

EXPRESSED IN BRAIN, SKIN AND PF  
BRAIN; ISOFORM 2 IN PROSTATE.

**SIMILARITY**

BELONGS TO PEPTIDASE FAMILY S1

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**Database cross-references**

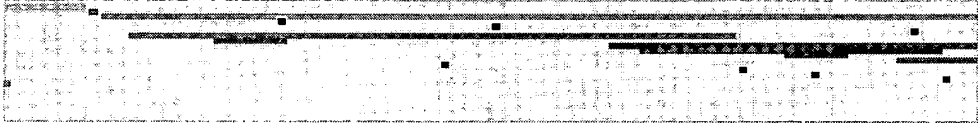
EMBL	<a href="#">AB012917</a> ; <a href="#">BAA33404.1</a> ; ALT_INIT.
	<a href="#">AB013730</a> ; <a href="#">BAA88713.1</a> ; -.
	<a href="#">AB041036</a> ; <a href="#">BAA96797.1</a> ; -.
	<a href="#">AF164623</a> ; <a href="#">AAD47815.1</a> ; -.
	<a href="#">AF243527</a> ; <a href="#">AAG33364.1</a> ; -.
	<a href="#">AC011473</a> ; <a href="#">AAG23257.1</a> ; -.
	<a href="#">BC022068</a> ; <a href="#">AAH22068.1</a> ; -.

HSSP	P00763; <u>1DPO</u> .
MEROPS	<u>S01.257</u> ; -.
Genew	HGNC: <u>6359</u> ; KLK11.
MIM	<u>604434</u> ; -.
InterPro	<u>IPR001314</u> ; Chymotrypsin. <u>IPR001254</u> ; Ser_protease_Try.
Pfam	<u>PF00089</u> ; trypsin; 1.
PRINTS	<u>PR00722</u> ; CHYMOTRYPSIN.
SMART	<u>SM00020</u> ; Tryp_SPc; 1.
	<u>PS50240</u> ; TRYPSIN_DOM; 1.
PROSITE	<u>PS00134</u> ; TRYPSIN_HIS; 1. <u>PS00135</u> ; TRYPSIN_SER; 1.

Keywords

Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen; Alternative

Features



Key	Begin	End	Length	Description
<u>SIGNAL</u>	1	18	18	POTENTIAL.
<u>PROPEP</u>	19	21	3	ACTIVATION PEPTIDE (POTENTIAL).
<u>CHAIN</u>	22	250	229	KALLIKREIN 11.
<u>ACT_SITE</u>	62	62	1	CHARGE RELAY SYSTEM (BY SIMILARITY)
<u>ACT_SITE</u>	110	110	1	CHARGE RELAY SYSTEM (BY SIMILARITY)
<u>ACT_SITE</u>	203	203	1	CHARGE RELAY SYSTEM (BY SIMILARITY)
<u>DISULFID</u>	28	163	136	BY SIMILARITY.
<u>DISULFID</u>	47	63	17	BY SIMILARITY.
<u>DISULFID</u>	135	237	103	BY SIMILARITY.
<u>DISULFID</u>	142	209	68	BY SIMILARITY.
<u>DISULFID</u>	174	188	15	BY SIMILARITY.
<u>DISULFID</u>	199	224	26	BY SIMILARITY.
<u>CARBOHYD</u>	99	99	1	N-LINKED (GLCNAC...) (POTENTIAL).
<u>CARBOHYD</u>	165	165	1	N-LINKED (GLCNAC...) (POTENTIAL).
<u>CARBOHYD</u>	181	181	1	N-LINKED (GLCNAC...) (POTENTIAL).
<u>CARBOHYD</u>	210	210	1	N-LINKED (GLCNAC...) (POTENTIAL).
<u>VARSPIC</u>	1	1	1	M -> MQRLRWLRDWKSSGRGLTAAKEP

Sequence information

Length: 250 aa, molecular weight: 27466 Da, CRC64 checksum: 192D910BB

MRILQLILLA LATGLVGGETRIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWL

Signal peptide      Activ peptide

AHCLKPRYIV HLGQHNQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVK  
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCEN/  
NITDTMVCAS VQEGGKDSCQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYT  
DWIQETMKNN 250

//

General	Description	References	Comments	Link
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